

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 10/774,378
Source: 1 Fw/b
Date Processed by STIC: 10/24/07

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 10/24/2007

PATENT APPLICATION: US/10/774,378

TIME: 11:56:15

Input Set : A:\10774378.txt

Output Set: N:\CRF4\10242007\J774378.raw

2 <110> APPLICANT: Ono Pharmaceutical Co., Ltd.

4 <120> TITLE OF INVENTION: Novel Polypeptides, DNAs encoding the polypeptides, and utility of the

5 Polypeptides

7 <130> FILE REFERENCE: Q55589

9 <140> CURRENT APPLICATION NUMBER: 10/774,378

10 <141> CURRENT FILING DATE: 2004-02-10

12 <150> PRIOR APPLICATION NUMBER: 09/380,276

13 <151> PRIOR FILING DATE: 1999-08-27

15 <150> PRIOR APPLICATION NUMBER: JP 9-43143

16 <151> PRIOR FILING DATE: 1997-02-27

18 <150> PRIOR APPLICATION NUMBER: PCT/JP98/00799

19 <151> PRIOR FILING DATE: 1997-02-27

21 <160> NUMBER OF SEQ ID NOS: 10

23 <170> SOFTWARE: PatentIn version 3.0

25 <210> SEQ ID NO: 1

26 <211> LENGTH: 1251

27 <212> TYPE: DNA

28 <213> ORGANISM: Homo Sapiens

30 <400> SEQUENCE: 1

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| 33 | ggctatattgt | catgtaaagt | gacttgtaga | acaggagact | gtagacagca | agaattcagg | 120 |
| 35 | gatcggctctg | gaaactgtgt | tccctgcaac | cagtgtgggc | cagggcatgga | gttgtctaag | 180 |
| 37 | gaatgtggct | tcggctatgg | ggaggatgca | cagtgtgtga | cgtgccggct | gcacagggtc | 240 |
| 39 | aaggaggact | ggggcttcca | gaaatgcaag | ccctgtctgg | actgcgcagt | ggtgaaccgc | 300 |
| 41 | tttcagaagg | caaattgttc | agccaccagt | gatgccatct | gcggggactg | cttgccagga | 360 |
| 43 | ttttatagga | agacgaaact | tgctcggcttt | caagacatgg | agtgtgtgcc | ttgtggagac | 420 |
| 45 | cctcctcctc | cttacgaacc | gcactgtgcc | agcaagggtca | acctcgtgaa | gatcgcgtcc | 480 |
| 47 | acggcctcca | gcccacggga | cacggcgctg | gctgccgtta | tctgcagcgc | tctggccacc | 540 |
| 49 | gtcctgctgg | ccctgctcat | cctctgtgtc | atctattgta | agagacagtt | tatggagaag | 600 |
| 51 | aaacccagct | ggtctctgcg | gtcacaggac | attcagtaca | acggctctga | gctgtcgtgt | 660 |
| 53 | cttgacagac | ctcagctcca | cgaatatgcc | cacagagcct | gctgccagtg | ccgccgtgac | 720 |
| 55 | tcagtgcaga | cctgcggggc | ggtgcgcttg | ctcccatcca | tgtgctgtga | ggaggcctgc | 780 |
| 57 | agccccaacc | cggcgactct | tggttgtggg | gtgcattctg | cagccagtct | tcaggcaaga | 840 |
| 59 | aacgcaggcc | cagccgggga | gatggtgccg | actttcttcg | gatccctcac | gcagtccatc | 900 |
| 61 | tgtggcgagt | tttcagatgc | ctggcctctg | atgcagaatc | ccatgggtgg | tgacaacatc | 960 |
| 63 | tctttttgtg | actcttatcc | tgaactcact | ggagaagaca | ttcattctct | caatccagaa | 1020 |
| 65 | cttgaaagct | caacgtcttt | ggattcaaat | agcagtcaag | atcttggttg | tggggctggt | 1080 |
| 67 | ccagtccagt | ctcattctga | aaactttaca | gcagctactg | atctatctag | atataacaac | 1140 |
| 69 | acactggtag | aatcagcatc | aactcaggat | gcactaacta | tgagaagcca | gctagatcag | 1200 |
| 71 | gagagtggcg | ctatcatcca | cccagccact | cagacgtccc | tccaggaagc | t | 1251 |

73 <210> SEQ ID NO: 2

74 <211> LENGTH: 1704

75 <212> TYPE: DNA

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Input Set : A:\10774378.txt

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76 <213> ORGANISM: Homo sapiens

78 <400> SEQUENCE: 2

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83 aagtgacttg tgaaacagga gactgtagac agcaagaatt cagggatcgg tctggaaact      180
85 gtgttccttg caaccagtgt gggccaggca tggagttgtc taaggaaatgt ggcttcggct      240
87 atggggagga tgcacagtgt gtgacgtgcc ggctgcacag gttcaaggag gactggggct      300
89 tccagaaatg caagccctgt ctggactgcg cagtggtgaa ccgctttcag aaggcaaatt      360
91 gttcagccac cagtgatgcc atctgcgggg actgcttgcc aggattttat aggaagacga      420
93 aacttgctcg ctttcaagac atggagtgtg tgccttggtg agaccctcct cctccttacg      480
95 aaccgcactg tgccagcaag gtcaacctcg tgaagatcgc gtccacggcc tccagcccac      540
97 gggacacggc gctggctgcc gttatctgca gcgctctggc caccgtcctg ctggccctgc      600
99 tcacctctg tgcatctat tgtaagagac agtttatgga gaagaaaccc agctggtctc      660
101 tgcggtcaca ggacattcag tacaacggct ctgagctgtc gtgtcttgac agacctcagc      720
103 tccacgaata tgcccacaga gcctgctgcc agtgccgccc tgactcagtg cagacctgcg      780
105 ggccggtgcg cttgctccca tccatgtgct gtgaggaggc ctgcagcccc aaccggcgga      840
107 ctcttggttg tggggtgcat tctgcagcca gtcttcaggc aagaaacgca ggcccagccg      900
109 gggagatggt gccgactttc ttcggatccc tcacgcagtc catctgtggc gagttttcag      960
111 atgcctggcc tctgatgcag aatcccatgg gtggtgacaa catctctttt tgtgactctt     1020
113 atcctgaact cactggagaa gacattcatt ctctcaatcc agaacttgaa agctcaacgt     1080
115 ctttggattc aaatagcagt caagatttgg ttggtggggc tgttccagtc cagtctcatt     1140
117 ctgaaaactt tacagcagct actgatttat ctagatataa caacacactg gtagaatcag     1200
119 catcaactca ggatgcacta actatgagaa gccagctaga tcaggagagt ggcgctatca     1260
121 tccaccagc cactcagacg tccctccagg aagcttaaag aacctgcttc tttctgcagt     1320
123 agaagcgtgt gctggaaccc aaagagtact cctttgttag gcttatggac tgagcagtct     1380
125 ggaccttgca tggcttctgg ggcaaaaata aatctgaacc aaactgacgg catttgaagc     1440
127 ctttcagcca gttgcttctg agccagacca gctgtaagct gaaacctcaa tgaataacaa     1500
129 gaaaagactc caggccgact catgatactc tgcattcttc ctacatgaga agcttctctg     1560
131 ccacaaaagt gacttcaaag acggatgggt tgagctggca gcctatgaga ttgtggacat     1620
133 ataacaagaa acagaaatgc cctcatgctt attttcatgg tgattgtggt tttacaagac     1680
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138 <210> SEQ ID NO: 3

139 <211> LENGTH: 1704

140 <212> TYPE: DNA

141 <213> ORGANISM: Homo sapiens

143 <220> FEATURE:

144 <221> NAME/KEY: misc_feature

145 <223> OTHER INFORMATION: Origin: human bone marrow stromal cell line HAS303

148 <220> FEATURE:

149 <221> NAME/KEY: CDS

150 <222> LOCATION: (45)..(1295)

152 <220> FEATURE:

153 <221> NAME/KEY: sig_peptide

154 <222> LOCATION: (45)..(119)

156 <220> FEATURE:

157 <221> NAME/KEY: mat_peptide

158 <222> LOCATION: (120)..(1295)

160 <400> SEQUENCE: 3

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 162 | | | | | | | | | | | | | | Met | Ala | Leu | Lys | |
| 163 | | | | | | | | | | | | | | -25 | | | | |
| 165 | gtg | cta | cta | gaa | caa | gag | aaa | acg | ttt | ttc | act | ctt | tta | gta | tta | cta | | 104 |
| 166 | Val | Leu | Leu | Glu | Gln | Glu | Lys | Thr | Phe | Phe | Thr | Leu | Leu | Val | Leu | Leu | | |
| 167 | | -20 | | | | | -15 | | | | | | -10 | | | | | |
| 169 | ggc | tat | ttg | tca | tgt | aaa | gtg | act | tgt | gaa | aca | gga | gac | tgt | aga | cag | | 152 |
| 170 | Gly | Tyr | Leu | Ser | Cys | Lys | Val | Thr | Cys | Glu | Thr | Gly | Asp | Cys | Arg | Gln | | |
| 171 | -5 | | | | -1 | 1 | | | | 5 | | | | | 10 | | | |
| 173 | caa | gaa | ttc | agg | gat | cgg | tct | gga | aac | tgt | gtt | ccc | tgc | aac | cag | tgt | | 200 |
| 174 | Gln | Glu | Phe | Arg | Asp | Arg | Ser | Gly | Asn | Cys | Val | Pro | Cys | Asn | Gln | Cys | | |
| 175 | | | | 15 | | | | | 20 | | | | | 25 | | | | |
| 177 | ggg | cca | ggc | atg | gag | ttg | tct | aag | gaa | tgt | ggc | ttc | ggc | tat | ggg | gag | | 248 |
| 178 | Gly | Pro | Gly | Met | Glu | Leu | Ser | Lys | Glu | Cys | Gly | Phe | Gly | Tyr | Gly | Glu | | |
| 179 | | | 30 | | | | | 35 | | | | | 40 | | | | | |
| 181 | gat | gca | cag | tgt | gtg | acg | tgc | cgg | ctg | cac | agg | ttc | aag | gag | gac | tgg | | 296 |
| 182 | Asp | Ala | Gln | Cys | Val | Thr | Cys | Arg | Leu | His | Arg | Phe | Lys | Glu | Asp | Trp | | |
| 183 | | 45 | | | | | 50 | | | | | 55 | | | | | | |
| 185 | ggc | ttc | cag | aaa | tgc | aag | ccc | tgt | ctg | gac | tgc | gca | gtg | gtg | aac | cgc | | 344 |
| 186 | Gly | Phe | Gln | Lys | Cys | Lys | Pro | Cys | Leu | Asp | Cys | Ala | Val | Val | Asn | Arg | | |
| 187 | 60 | | | | | 65 | | | | | 70 | | | | 75 | | | |
| 189 | ttt | cag | aag | gca | aat | tgt | tca | gcc | acc | agt | gat | gcc | atc | tgc | ggg | gac | | 392 |
| 190 | Phe | Gln | Lys | Ala | Asn | Cys | Ser | Ala | Thr | Ser | Asp | Ala | Ile | Cys | Gly | Asp | | |
| 191 | | | | | 80 | | | | 85 | | | | | 90 | | | | |
| 193 | tgc | ttg | cca | gga | ttt | tat | agg | aag | acg | aaa | ctt | gtc | ggc | ttt | caa | gac | | 440 |
| 194 | Cys | Leu | Pro | Gly | Phe | Tyr | Arg | Lys | Thr | Lys | Leu | Val | Gly | Phe | Gln | Asp | | |
| 195 | | | | 95 | | | | | 100 | | | | | 105 | | | | |
| 197 | atg | gag | tgt | gtg | cct | tgt | gga | gac | cct | cct | cct | cct | tac | gaa | ccg | cac | | 488 |
| 198 | Met | Glu | Cys | Val | Pro | Cys | Gly | Asp | Pro | Pro | Pro | Pro | Tyr | Glu | Pro | His | | |
| 199 | | | 110 | | | | | 115 | | | | | 120 | | | | | |
| 201 | tgt | gcc | agc | aag | gtc | aac | ctc | gtg | aag | atc | gcg | tcc | acg | gcc | tcc | agc | | 536 |
| 202 | Cys | Ala | Ser | Lys | Val | Asn | Leu | Val | Lys | Ile | Ala | Ser | Thr | Ala | Ser | Ser | | |
| 203 | | 125 | | | | | 130 | | | | | 135 | | | | | | |
| 205 | cca | cgg | gac | acg | gcg | ctg | gct | gcc | gtt | atc | tgc | agc | gct | ctg | gcc | acc | | 584 |
| 206 | Pro | Arg | Asp | Thr | Ala | Leu | Ala | Ala | Val | Ile | Cys | Ser | Ala | Leu | Ala | Thr | | |
| 207 | 140 | | | | | 145 | | | | | 150 | | | | 155 | | | |
| 209 | gtc | ctg | ctg | gcc | ctg | ctc | atc | ctc | tgt | gtc | atc | tat | tgt | aag | aga | cag | | 632 |
| 210 | Val | Leu | Leu | Ala | Leu | Leu | Ile | Leu | Cys | Val | Ile | Tyr | Cys | Lys | Arg | Gln | | |
| 211 | | | | | 160 | | | | 165 | | | | | 170 | | | | |
| 213 | ttt | atg | gag | aag | aaa | ccc | agc | tgg | tct | ctg | cgg | tca | cag | gac | att | cag | | 680 |
| 214 | Phe | Met | Glu | Lys | Lys | Pro | Ser | Trp | Ser | Leu | Arg | Ser | Gln | Asp | Ile | Gln | | |
| 215 | | | | 175 | | | | | 180 | | | | | 185 | | | | |
| 217 | tac | aac | ggc | tct | gag | ctg | tcg | tgt | ctt | gac | aga | cct | cag | ctc | cac | gaa | | 728 |
| 218 | Tyr | Asn | Gly | Ser | Glu | Leu | Ser | Cys | Leu | Asp | Arg | Pro | Gln | Leu | His | Glu | | |
| 219 | | | 190 | | | | | 195 | | | | | 200 | | | | | |
| 221 | tat | gcc | cac | aga | gcc | tgc | tgc | cag | tgc | cgc | cgt | gac | tca | gtg | cag | acc | | 776 |
| 222 | Tyr | Ala | His | Arg | Ala | Cys | Cys | Gln | Cys | Arg | Arg | Asp | Ser | Val | Gln | Thr | | |
| 223 | | 205 | | | | | 210 | | | | | 215 | | | | | | |
| 225 | tgc | ggg | ccg | gtg | cgc | ttg | ctc | cca | tcc | atg | tgc | tgt | gag | gag | gcc | tgc | | 824 |
| 226 | Cys | Gly | Pro | Val | Arg | Leu | Leu | Pro | Ser | Met | Cys | Cys | Glu | Glu | Ala | Cys | | |

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/774,378

DATE: 10/24/2007

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Input Set : A:\10774378.txt

Output Set: N:\CRF4\10242007\J774378.raw

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227 220                225                230                235
229 agc ccc aac ccg gcg act ctt ggt tgt ggg gtg cat tct gca gcc agt      872
230 Ser Pro Asn Pro Ala Thr Leu Gly Cys Gly Val His Ser Ala Ala Ser
231                240                245                250
233 ctt cag gca aga aac gca ggc cca gcc ggg gag atg gtg ccg act ttc      920
234 Leu Gln Ala Arg Asn Ala Gly Pro Ala Gly Glu Met Val Pro Thr Phe
235                255                260                265
237 ttc gga tcc ctc acg cag tcc atc tgt ggc gag ttt tca gat gcc tgg      968
238 Phe Gly Ser Leu Thr Gln Ser Ile Cys Gly Glu Phe Ser Asp Ala Trp
239                270                275                280
241 cct ctg atg cag aat ccc atg ggt ggt gac aac atc tct ttt tgt gac      1016
242 Pro Leu Met Gln Asn Pro Met Gly Gly Asp Asn Ile Ser Phe Cys Asp
243                285                290                295
245 tct tat cct gaa ctc act gga gaa gac att cat tct ctc aat cca gaa      1064
246 Ser Tyr Pro Glu Leu Thr Gly Glu Asp Ile His Ser Leu Asn Pro Glu
247 300                305                310                315
249 ctt gaa agc tca acg tct ttg gat tca aat agc agt caa gat ttg gtt      1112
250 Leu Glu Ser Ser Thr Ser Leu Asp Ser Asn Ser Ser Gln Asp Leu Val
251                320                325                330
253 ggt ggg gct gtt cca gtc cag tct cat tct gaa aac ttt aca gca gct      1160
254 Gly Gly Ala Val Pro Val Gln Ser His Ser Glu Asn Phe Thr Ala Ala
255                335                340                345
257 act gat tta tct aga tat aac aac aca ctg gta gaa tca gca tca act      1208
258 Thr Asp Leu Ser Arg Tyr Asn Asn Thr Leu Val Glu Ser Ala Ser Thr
259                350                355                360
261 cag gat gca cta act atg aga agc cag cta gat cag gag agt ggc gct      1256
262 Gln Asp Ala Leu Thr Met Arg Ser Gln Leu Asp Gln Glu Ser Gly Ala
263                365                370                375
265 atc atc cac cca gcc act cag acg tcc ctc cag gaa gct taaagaacct      1305
266 Ile Ile His Pro Ala Thr Gln Thr Ser Leu Gln Glu Ala
267 380                385                390
269 gcttcttttct gcagtagaag cgtgtgctgg aaccctaaaga gtactccttt gttaggctta      1365
271 tggactgagc agtctggacc ttgcatggct tctggggcaa aaataaatct gaaccaaact      1425
273 gacggcattt gaagcctttc agccagttgc ttctgagcca gaccagctgt aagctgaaac      1485
275 ctcaatgaat aacaagaaaa gactccaggc cgactcatga tactctgcat ctttcctaca      1545
277 tgagaagctt ctctgccaca aaagtgactt caaagacgga tggggttgagc tggcagccta      1605
279 tgagattgtg gacatataac aagaaacaga aatgccctca tgcttatttt catggtgatt      1665
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285 <211> LENGTH: 417
286 <212> TYPE: PRT
287 <213> ORGANISM: Homo sapiens
289 <220> FEATURE:
290 <221> NAME/KEY: misc_feature
291 <223> OTHER INFORMATION: Origin: human bone marrow stromal cell line HAS303
293 <400> SEQUENCE: 4
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299 Leu Val Leu Leu Gly Tyr Leu Ser Cys Lys Val Thr Cys Glu Thr Gly

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| 304 | | | | 10 | | | | 15 | | | | 20 | | | | |
| 307 | Cys | Asn | Gln | Cys | Gly | Pro | Gly | Met | Glu | Leu | Ser | Lys | Glu | Cys | Gly | Phe |
| 308 | | 25 | | | | | 30 | | | | | 35 | | | | |
| 311 | Gly | Tyr | Gly | Glu | Asp | Ala | Gln | Cys | Val | Thr | Cys | Arg | Leu | His | Arg | Phe |
| 312 | 40 | | | | | 45 | | | | | 50 | | | | 55 | |
| 315 | Lys | Glu | Asp | Trp | Gly | Phe | Gln | Lys | Cys | Lys | Pro | Cys | Leu | Asp | Cys | Ala |
| 316 | | | | 60 | | | | | | 65 | | | | | 70 | |
| 319 | Val | Val | Asn | Arg | Phe | Gln | Lys | Ala | Asn | Cys | Ser | Ala | Thr | Ser | Asp | Ala |
| 320 | | | | 75 | | | | | 80 | | | | | 85 | | |
| 323 | Ile | Cys | Gly | Asp | Cys | Leu | Pro | Gly | Phe | Tyr | Arg | Lys | Thr | Lys | Leu | Val |
| 324 | | | 90 | | | | | 95 | | | | | 100 | | | |
| 327 | Gly | Phe | Gln | Asp | Met | Glu | Cys | Val | Pro | Cys | Gly | Asp | Pro | Pro | Pro | Pro |
| 328 | | 105 | | | | | | 110 | | | | 115 | | | | |
| 331 | Tyr | Glu | Pro | His | Cys | Ala | Ser | Lys | Val | Asn | Leu | Val | Lys | Ile | Ala | Ser |
| 332 | 120 | | | | | 125 | | | | | 130 | | | | | 135 |
| 335 | Thr | Ala | Ser | Ser | Pro | Arg | Asp | Thr | Ala | Leu | Ala | Ala | Val | Ile | Cys | Ser |
| 336 | | | | 140 | | | | | | 145 | | | | | 150 | |
| 339 | Ala | Leu | Ala | Thr | Val | Leu | Leu | Ala | Leu | Leu | Ile | Leu | Cys | Val | Ile | Tyr |
| 340 | | | | 155 | | | | | 160 | | | | | 165 | | |
| 343 | Cys | Lys | Arg | Gln | Phe | Met | Glu | Lys | Lys | Pro | Ser | Trp | Ser | Leu | Arg | Ser |
| 344 | | | 170 | | | | | 175 | | | | | 180 | | | |
| 347 | Gln | Asp | Ile | Gln | Tyr | Asn | Gly | Ser | Glu | Leu | Ser | Cys | Leu | Asp | Arg | Pro |
| 348 | | 185 | | | | 190 | | | | | | 195 | | | | |
| 351 | Gln | Leu | His | Glu | Tyr | Ala | His | Arg | Ala | Cys | Cys | Gln | Cys | Arg | Arg | Asp |
| 352 | 200 | | | | | 205 | | | | | 210 | | | | | 215 |
| 355 | Ser | Val | Gln | Thr | Cys | Gly | Pro | Val | Arg | Leu | Leu | Pro | Ser | Met | Cys | Cys |
| 356 | | | | 220 | | | | | | 225 | | | | | 230 | |
| 359 | Glu | Glu | Ala | Cys | Ser | Pro | Asn | Pro | Ala | Thr | Leu | Gly | Cys | Gly | Val | His |
| 360 | | | | 235 | | | | | 240 | | | | | 245 | | |
| 363 | Ser | Ala | Ala | Ser | Leu | Gln | Ala | Arg | Asn | Ala | Gly | Pro | Ala | Gly | Glu | Met |
| 364 | | | 250 | | | | | 255 | | | | | 260 | | | |
| 367 | Val | Pro | Thr | Phe | Phe | Gly | Ser | Leu | Thr | Gln | Ser | Ile | Cys | Gly | Glu | Phe |
| 368 | | 265 | | | | 270 | | | | | | 275 | | | | |
| 371 | Ser | Asp | Ala | Trp | Pro | Leu | Met | Gln | Asn | Pro | Met | Gly | Gly | Asp | Asn | Ile |
| 372 | 280 | | | | | 285 | | | | | 290 | | | | | 295 |
| 375 | Ser | Phe | Cys | Asp | Ser | Tyr | Pro | Glu | Leu | Thr | Gly | Glu | Asp | Ile | His | Ser |
| 376 | | | | 300 | | | | | | 305 | | | | | 310 | |
| 379 | Leu | Asn | Pro | Glu | Leu | Glu | Ser | Ser | Thr | Ser | Leu | Asp | Ser | Asn | Ser | Ser |
| 380 | | | | 315 | | | | | 320 | | | | | 325 | | |
| 383 | Gln | Asp | Leu | Val | Gly | Gly | Ala | Val | Pro | Val | Gln | Ser | His | Ser | Glu | Asn |
| 384 | | | 330 | | | | | 335 | | | | | 340 | | | |
| 387 | Phe | Thr | Ala | Ala | Thr | Asp | Leu | Ser | Arg | Tyr | Asn | Asn | Thr | Leu | Val | Glu |
| 388 | | 345 | | | | 350 | | | | | | 355 | | | | |
| 391 | Ser | Ala | Ser | Thr | Gln | Asp | Ala | Leu | Thr | Met | Arg | Ser | Gln | Leu | Asp | Gln |
| 392 | 360 | | | | | 365 | | | | | 370 | | | | 375 | |
| 395 | Glu | Ser | Gly | Ala | Ile | Ile | His | Pro | Ala | Thr | Gln | Thr | Ser | Leu | Gln | Glu |
| 396 | | | | 380 | | | | | | 385 | | | | | 390 | |

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:9; N Pos. 27,28,29,30,31,32,33,34,35

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:9,10

VERIFICATION SUMMARY

DATE: 10/24/2007

PATENT APPLICATION: US/10/774,378

TIME: 11:56:16

Input Set : A:\10774378.txt

Output Set: N:\CRF4\10242007\J774378.raw

L:786 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:9

L:786 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0